Resource Summary Report

Generated by RRID on Apr 18, 2025

Mikado

RRID:SCR_016159
Type: Tool

Proper Citation

Mikado (RRID:SCR_016159)

Resource Information

URL: https://github.com/lucventurini/mikado/

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Description: Mikado is a lightweight Python3 pipeline whose purpose is to facilitate the identification of expressed loci from RNA-Seq data * and to select the best models in each locus.

Resource Type: source code, software resource

Defining Citation: DOI:10.1101/216994

Keywords: annotation, rna-seq, genomics, transcriptomics

Funding: BBSRC BB/J004669/1;
BBSRC BB/J010375/1;
BBSRC BB/CSP17270/1;
BBSRC BB/CCG1720/1

Availability: Free, Available for download

Resource Name: Mikado

Resource ID: SCR_016159

Alternate URLs: http://mikado.readthedocs.io/

License: LGPL 3, gnu lesser general public license

License URLs: https://github.com/lucventurini/mikado/blob/master/LICENSE.txt

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250412T060004+0000

Ratings and Alerts

No rating or validation information has been found for Mikado.

No alerts have been found for Mikado.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Low EL, et al. (2024) Chromosome-scale Elaeis guineensis and E. oleifera assemblies: comparative genomics of oil palm and other Arecaceae. G3 (Bethesda, Md.), 14(9).

Chang X, et al. (2024) High-quality Gossypium hirsutum and Gossypium barbadense genome assemblies reveal the landscape and evolution of centromeres. Plant communications, 5(2), 100722.

Marlétaz F, et al. (2024) The hagfish genome and the evolution of vertebrates. Nature, 627(8005), 811.

Fuertes-Rabanal M, et al. (2024) Linear ?-1,2-glucans trigger immune hallmarks and enhance disease resistance in plants. Journal of experimental botany, 75(22), 7337.

Liu H, et al. (2024) The genome of Eleocharis vivipara elucidates the genetics of C3-C4 photosynthetic plasticity and karyotype evolution in the Cyperaceae. Journal of integrative plant biology, 66(11), 2505.

Wright J, et al. (2024) Chromosome-scale genome assembly and de novo annotation of Alopecurus aequalis. Scientific data, 11(1), 1368.

Grewal S, et al. (2024) Chromosome-scale genome assembly of bread wheat's wild relative Triticum timopheevii. Scientific data, 11(1), 420.

Bista B, et al. (2024) De novo genome assemblies of two cryptodiran turtles with ZZ/ZW and

XX/XY sex chromosomes provide insights into patterns of genome reshuffling and uncover novel 3D genome folding in amniotes. Genome research, 34(10), 1553.

Sarre LA, et al. (2024) DNA methylation enables recurrent endogenization of giant viruses in an animal relative. Science advances, 10(28), eado6406.

Nash WJ, et al. (2024) The genome sequence of the Violet Carpenter Bee, Xylocopa violacea (Linnaeus, 1785): a hymenopteran species undergoing range expansion. Heredity, 133(6), 381.

Shippy TD, et al. (2024) Diaci v3.0: chromosome-level assembly, de novo transcriptome, and manual annotation of Diaphorina citri, insect vector of Huanglongbing. GigaScience, 13.

Guedes JG, et al. (2024) The leaf idioblastome of the medicinal plant Catharanthus roseus is associated with stress resistance and alkaloid metabolism. Journal of experimental botany, 75(1), 274.

McElroy KE, et al. (2024) A chromosome-level genome assembly of the disco clam, Ctenoides ales. G3 (Bethesda, Md.), 14(9).

Carpinteyro-Ponce J, et al. (2024) The Complex Landscape of Structural Divergence Between the Drosophila pseudoobscura and D. persimilis Genomes. Genome biology and evolution, 16(3).

Wei J, et al. (2024) Chromosome-level genome assembly of the silver pomfret Pampus argenteus. Scientific data, 11(1), 234.

Cicconardi F, et al. (2024) Novel Sex-Specific Genes and Diverse Interspecific Expression in the Antennal Transcriptomes of Ithomiine Butterflies. Genome biology and evolution, 16(10).

Guan L, et al. (2024) Tert-expressing cells contribute to salivary gland homeostasis and tissue regeneration after radiation therapy. Genes & development, 38(11-12), 569.

Arick MA, et al. (2023) A high-quality chromosome-level genome assembly of rohu carp, Labeo rohita, and its utilization in SNP-based exploration of gene flow and sex determination. G3 (Bethesda, Md.), 13(3).

Dadras A, et al. (2023) Environmental gradients reveal stress hubs pre-dating plant terrestrialization. Nature plants, 9(9), 1419.

McGowan J, et al. (2023) Identification of a non-canonical ciliate nuclear genetic code where UAA and UAG code for different amino acids. PLoS genetics, 19(10), e1010913.